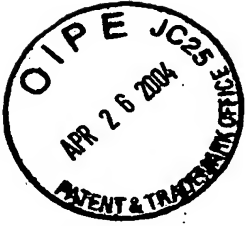


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```
1  GTCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTCTCTCTGCTCGCCCGCTG 60
   -----+-----+-----+-----+-----+-----+-----+
   CAGGAAGGTGGTACGTGAGCGACCCGAAGAAGAGACACCGCACAAAGAGACGAGCGCGGAC
       M H S L G F F S V A C S L L A A A -
61  CGCTGCTCCCGGTCTCGCGAGGCGCGCGCGCGCGCGCTTCGAGTCCGGACTCG 120
   -----+-----+-----+-----+-----+-----+-----+
   GCGACGAGGCGCCAGGAGCGCTCCGCGGCGCGCGCGCGGCGGAGCTCAGGCCCTGAGC
       L L P G P R E A P A A A A A F E S G L D -
121 ACCTCTCGGACGCGGAGCCCGACGCGGCGGAGGCCACGGCTTATGCAAGCAAGATCTGG 180
   -----+-----+-----+-----+-----+-----+-----+
   TGGAGAGCCTGCGCCTCGGGCTGCGCCCGCTCCGGTGCGCGAATACGTTCTGTTCTAGACC
       L S D A E P D A G E A T A Y A S K D L E -
181 AGGAGCAGTTACGGTCTGTGTCCAGTGATGAAGTCACTGACTGTACTCTACCCAGAAT 240
   -----+-----+-----+-----+-----+-----+-----+
   TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA
       E Q L R S V S S V D E L M T V L Y P E Y -
241 ATTGGAAAATGTACAAGTGCAGCTAAGGAAGGAGGCTGGCAACATAACAGAGAACAGG 300
   -----+-----+-----+-----+-----+-----+-----+
   TAACCTTTTACATGTTACAGTCGATTCTCTTCCCTCCGACCGTTGTATTGTCTCTGTCC
       W K M Y K C Q L R K G G W Q H N R E Q A -
   CCAACCTCAACTCAAGGACAGAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG
```

Fig. 1A



360  
GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATATATGTC  
N L N S R T E E T I K F A A A H Y N T E -  
361  
AGATCTTGAAAAGTATTGATAATGAGTGGAGAAAGACTCAATGCATGCCACGGGAGGTGT  
TCTAGAACTTTTCATAAAGTATTACTCACCCTCTTCTGAGTTACGTACGGTGCCCTCCACA  
I L K S I D N E W R K T Q C M P R E V C -  
421  
GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG  
CATATCTACACCCCTTCTCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACAC  
I D V G K E F G V A T N T F F K P P C V -  
541  
TGTCCGTCTACAGATGTGGGGGTGCTGCAATAGTGAGGGCTGCAGTGCATGAACACCA  
ACAGGCAGATGTCTACACCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT  
S V Y R C G C C N S E G L Q C M N T S -  
541  
GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCCTCTCTCAAGGCCCA  
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGATTCCGGGGT  
T S Y L S K T L F E I T V P L S Q G P K -  
660  
AACCAGTAACAATCAGTTTGTGCCAATCACACTTCCTGCCGATGCATGCTAAACTGGATG  
TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTGACCTAC  
P V T I S F A N H T S C R C M S K L D V -

Fig. 1B



661 TTTACAGACAAGTTTCATTCCATTATTAGACGTTCCCTGCCAGCAACACTACCACAGTGTC 720  
-----+-----+-----+-----+-----+-----+-----+  
AAATGTCTGTTCAAAGTAAGGTAATAATCTGCAAGGACGGTCGTTGTGATGGTGTACACAG  
Y R Q V H S I I R R S L P A T L P Q C Q -  
-----+-----+-----+-----+-----+-----+-----+  
721 AGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGGAATAATCACATCTGCAGATGCC 780  
-----+-----+-----+-----+-----+-----+-----+  
TCCGTCGCTTGTCTGGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGCTCTACCG  
A A N K T C P T N Y M W N N H I C R C L -  
-----+-----+-----+-----+-----+-----+-----+  
781 TGGCTCAGGAAGATTTTATGTTTCCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC 840  
-----+-----+-----+-----+-----+-----+-----+  
ACCGAGTCCTTCTAAATAACAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG  
A Q E D F M F S S D A G D S T D G F H -  
-----+-----+-----+-----+-----+-----+-----+  
841 ATGACATCTGTGGACCAACAAGGAGCTGGATGAAGAGACCTGTCTCAGTGTGTCTGCAGAG 900  
-----+-----+-----+-----+-----+-----+-----+  
TACTGTAGACACCTGGTTGTTCCTCGACCTACTTCTCTGGACAGTCAACACAGACGTCTC  
D I C G P N K E L D E E T C Q C V C R A -  
-----+-----+-----+-----+-----+-----+-----+  
901 CGGGCTTCGGCTGCCAGCTGTGGACCCCAAGAACTAGACAGAACTCATGCCAGT 960  
-----+-----+-----+-----+-----+-----+-----+  
GCCCCGAGCCGGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTACGGTCA  
G L R P A S C G P H K E L D R N S C Q C -  
-----+-----+-----+-----+-----+-----+-----+  
961 GTGTCTGTAAAAACAACCTCTTCCCCAGCCAATGTGGGGCCAAACCGAGAAATTGTATGAAA 1020  
-----+-----+-----+-----+-----+-----+-----+  
CACAGACATTTTGTGTGAGAAAGGGTCGGTTACACCCCGGTGGCTCTTAAACTACTTT

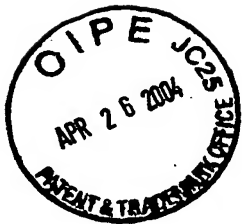
Fig.1C



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V C K N K L F P S Q C G A N R E F D E N -  
ACACATGCCAGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA 1080  
TGTTACGGTCCACACATACATTTCTTGGACGGGCTCTTAGTGGGATTTAGGACCTT  
T C C Q C V C K R T C P R N Q P L N P G K -  
AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGGAAAGAGTTCC 1140  
TTACACGGACACTTACATGTCTTTCAGGTGCTCTTACGAACAATTTCCCTTCTCAAGG  
C A C E C T E S P Q K C L L K G K K F H -  
ACCACCAACATGCAGCTGTACAGACGGCCATGTACGAACCCGACAGAAAGGCTTGTGAGC 1200  
TGGTGGTTGTGACGTCGACAAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAACACTCG  
H Q T C S C Y R R P C T N R Q K A C E P -  
CAGGATTTTCATATAGTGAAGAAGTGTGTCGTTGTGTCCTTCAATATTGGCAAAGACCAC 1260  
GTCCATAAAGTATATCACTTCTTACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG  
G F S Y S E E V C R C V P S Y W Q R P Q -  
AAATGAGCTAAGATTGTACTGTTTCCAGTTCATCGATTTTCTATTATGGAAAACTGTGT

Fig. 1D



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1320

1261  
-----+-----+-----+-----+  
TTTACTCGATTCTAACATGACAAAAGGTCAAGTAGCTAAAAGATAATACCTTTTGACACA

54

TGCCACAGTAGAACTGCTGTGTGAACAGAGAGACCCCTTGTGGGTCCATGCTAACAAAGACA 1380

1321 -----+-----+-----  
ACGGTGTCATCTTGACAGACACTTGTCTCTCTGGGAACCCAGGTA CGATTGTTTCTGT

ACGGTGCATCTTACAGGAGCTCTG  
AAAGTCTGTCTTTCTCCGAACCATGTGGATACTTTACAGAAAATGGACTGGAGCTCATCTG  
+-----+ 1440

1381  
-----+-----  
TTTCAGACAGAAGGACTTGGTACACCTATTGAAATGTCTTACC TGACCCTCGAGTAGAC

CAAAGGCCCTCTTGTAAGACTGGTTTCTGCCAATGACCAACAGCCCAAGATTTCCTC

1441  
-----+-----+-----+  
GTTTCCGGAGAACATTCTGACCAAAAGACGGTACTGGTTGTCTCGGTTCTAAAGGAG

TTGTGATTTCTTTAAAGAATGACTATATAATTATTTCCCACTAAATAATATGTTTCTGCG

1501      - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +  
AACACTAAAGAAATTTCTTACTGATATATTAATAAAGGTGATTTTATAACAAAGACG

ATTCA TTTTATAGCAACAACAATTGGTAAACTCAGTGATCAATATTTTATATCAT 1620

1561 TAAGTAAAAATATCGTGTGTTAACCATTGTGAGTGACACTAGTTATAAAAAATATAGTA

GCAGAAATATGTTTAAAAATAAAAATGAAAAATTGTATTATTATAAAAAAAA  
1674

1621  
-----+-----+  
CGTTTATACAAATTTTATTCTTTTACATAAATAATTTTCTTTT

Fig. 1E